WHAT IS CLAIMED IS:

1. A method for detection of a target nucleic acid sequence in a mixture of different nucleic acids having additional binding sites, the method comprising:

A) hybridizing the target nucleic acid sequence with a probe in liquid phase, the probe having a first label,

A1) hybridizing the additional binding sites with single stranded nucleic acids having random primary sequences in liquid phase,

B) separating the different nucleic acids, and

C) detecting the target nucleic acid by using the labeled probe.

2. Method according to claim 1,

- wherein short nucleic acids having a length of 6 to 12 nucleotides are provided in A1) for hybridizing.

3. Method according to claim 1,

- wherein hybridizing in A1) is carried out at roughly room temperature, and

- hybridizing in A) is carried out at a temperature between 56°C to 72°C.

4. Method according to claim 1,

- wherein a nucleic acid with a length of at least 10-times the length of the single stranded nucleic acids with random primary sequence is used as a probe,

- wherein A1) and A) are carried out simultaneously.

5. Method according to claim 2,

- wherein in A1) nucleic acids labeled with a second label are used for hybridizing,
- the second label being different from the first label.

6. Method according to claim 2,

- wherein the nucleic acids used for hybridizing in A1) are subsequently labeled with a second label after A1),
- the second label being different from the first label.

7. Method according to claim 1, comprising at least one of:

- prior to A) the mixture of different nucleic acids is denatured in a A2); and
- in A) a nucleic acid is used as a probe, having a stretch of 18 to 25 nucleotides being able to hybridize with the target nucleic acid sequence, this stretch having at least 80% sequence homology to the complementary sequence of the target nucleic acid sequence.

8. Method according to claim 1, comprising at least one of:

- in B) the nucleic acids are separated according to their mass by using a gel electrophorese; and
- in B) a microfluidic chip having capillaries suitable for nucleic acid electrophorese is used for separation.

9. Method according to claim 1,

- wherein a first and if present a second label is used, each being selected from the following group:

- radioactive labels, fluorescent markers, chemoluminescence, bioluminescence, magnetic labels and antigen labels.

10. Method according to claim 9,

- wherein fluorescent markers are used as the first and if present second label,

- the fluorescent markers of the first and second label emitting radiation of different wavelengths.

11. Method according to claim 10,

- wherein in C) the amount and the size of the hybrid strand of the target nucleic acid and the probe is determined via the first label and in case the second label is present, the amount of the other different nucleic acids in the mixture is determined via the second label,

- using a spectrometer for the detection of both labels.

12. A kit for performing a separation method according to claim 1, comprising:

- a probe labeled with a first label, able to hybridize with a target nucleic acid sequence,

- oligonucleotides with a randomized primary sequence for hybridizing to the additional binding sites present in the mixture of nucleic acids,

- a mass separator for separating nucleic acids according to their mass.

13. Kit according to the previous claim, comprising at least one of:

- the mass separator comprises a microfluidic chip; and

- a second label for labeling the oligonucleotides with randomized primary sequence.